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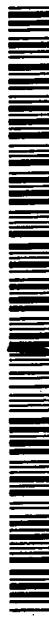
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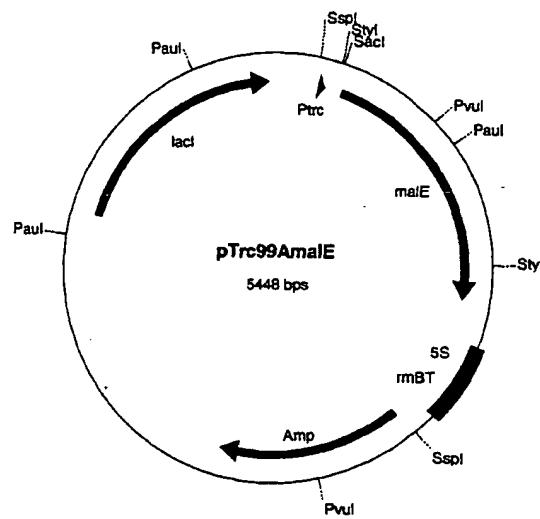
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(54) Title: PROCESS FOR THE PREPARATION OF L-AMINO ACIDS USING STRAINS OF THE ENTEROBACTERIACEAE FAMILY WHICH CONTAIN AN ENHANCED malE GENE



WO 03/008605 A2



(57) Abstract: The invention relates to a process for the preparation of L-amino acids, in particular L-threonine, in which the following steps are carried out: a) fermentation of microorganisms of the Enterobacteriaceae family which produce the desired L-amino acid and in which at least the malE gene, or the nucleotide sequence which codes for this, is or are enhanced, in particular over-expressed, b) concentration of the desired L-amino acid in the medium or in the cells of the bacteria, and c) isolation of the desired L-amino acid.

**Process for the Preparation of L-Amino Acids using
Strains of the Enterobacteriaceae Family which Contain
an Enhanced *male* Gene**

Field of the Invention

5 This invention relates to a process for the preparation of L-amino acids, in particular L-threonine, using strains of the Enterobacteriaceae family in which at least the *male* gene is enhanced.

Prior Art

10 L-Amino acids, in particular L-threonine, are used in human medicine and in the pharmaceuticals industry, in the foodstuffs industry and very particularly in animal nutrition.

It is known to prepare L-amino acids by fermentation of 15 strains of Enterobacteriaceae, in particular *Escherichia coli* (*E. coli*) and *Serratia marcescens*. Because of their great importance, work is constantly being undertaken to improve the preparation processes. Improvements to the process can relate to fermentation measures, such as e.g.

20 stirring and supply of oxygen, or the composition of the nutrient media, such as e.g. the sugar concentration during the fermentation, or the working up to the product form, by e.g. ion exchange chromatography, or the intrinsic output properties of the microorganism itself.

25 Methods of mutagenesis, selection and mutant selection are used to improve the output properties of these microorganisms. Strains which are resistant to antimetabolites, such as e.g. the threonine analogue α -amino- β -hydroxyvaleric acid (AHV), or are auxotrophic for 30 metabolites of regulatory importance and produce L-amino acid, such as e.g. L-threonine, are obtained in this manner.

Methods of the recombinant DNA technique have also been employed for some years for improving the strain of strains of the Enterobacteriaceae family which produce L-amino acids, by amplifying individual amino acid

5 biosynthesis genes and investigating the effect on the production.

Object of the Invention

The object of the invention is to provide new measures for improved fermentative preparation of L-amino acids, in

10 particular L-threonine.

Summary of the Invention

The invention provides a process for the fermentative preparation of L-amino acids, in particular L-threonine, using microorganisms of the Enterobacteriaceae family which

15 in particular already produce L-amino acids and in which at least the nucleotide sequence which codes for the *malE* gene is enhanced.

Detailed Description of the Invention

Where L-amino acids or amino acids are mentioned in the following, this means one or more amino acids, including their salts, chosen from the group consisting of L-asparagine, L-threonine, L-serine, L-glutamate, L-glycine, L-alanine, L-cysteine, L-valine, L-methionine, L-isoleucine, L-leucine, L-tyrosine, L-phenylalanine, L-histidine, L-lysine, L-tryptophan and L-arginine. L-Threonine is particularly preferred.

The term "enhancement" in this connection describes the increase in the intracellular activity of one or more enzymes or proteins in a microorganism which are coded by the corresponding DNA, for example by increasing the number of copies of the gene or genes, using a potent promoter or a gene or allele which codes for a corresponding enzyme or

protein with a high activity, and optionally combining these measures.

By enhancement measures, in particular over-expression, the activity or concentration of the corresponding protein is 5 in general increased by at least 10%, 25%, 50%, 75%, 100%, 150%, 200%, 300%, 400% or 500%, up to a maximum of 1000% or 2000%, based on that of the wild-type protein or the activity or concentration of the protein in the starting microorganism.

10 The process comprises carrying out the following steps:

- a) fermentation of microorganisms of the Enterobacteriaceae family in which at least the malE gene is enhanced,
- b) concentration of the corresponding L-amino acid in 15 the medium or in the cells of the microorganisms of the Enterobacteriaceae family, and
- c) isolation of the desired L-amino acid, constituents of the fermentation broth and/or the biomass in its entirety or portions (> 0 to 100 %) thereof 20 optionally remaining in the product.

The microorganisms which the present invention provides can produce L-amino acids from glucose, sucrose, lactose, fructose, maltose, molasses, optionally starch, optionally cellulose or from glycerol and ethanol. They are 25 representatives of the Enterobacteriaceae family chosen from the genera Escherichia, Erwinia, Providencia and Serratia. The genera Escherichia and Serratia are preferred. Of the genus Escherichia the species Escherichia coli and of the genus Serratia the species Serratia 30 marcescens are to be mentioned in particular.

Suitable strains, which produce L-threonine in particular, of the genus *Escherichia*, in particular of the species *Escherichia coli*, are, for example

5 *Escherichia coli* TF427
 Escherichia coli H4578
 Escherichia coli KY10935
 Escherichia coli VNIIgenetika MG442
 Escherichia coli VNIIgenetika M1
 Escherichia coli VNIIgenetika 472T23
10 *Escherichia coli* BKIIM B-3996
 Escherichia coli kat 13
 Escherichia coli KCCM-10132.

Suitable L-threonine-producing strains of the genus *Serratia*, in particular of the species *Serratia marcescens*,
15 are, for example

Serratia marcescens HNr21
Serratia marcescens TLr156
Serratia marcescens T2000.

Strains from the Enterobacteriaceae family which produce L-
20 threonine preferably have, inter alia, one or more genetic
or phenotypic features chosen from the group consisting of:
resistance to α -amino- β -hydroxyvaleric acid, resistance to
thialysine, resistance to ethionine, resistance to α -
methylserine, resistance to diaminosuccinic acid,
25 resistance to α -aminobutyric acid, resistance to
borrelidin, resistance to rifampicin, resistance to valine
analogues, such as, for example, valine hydroxamate,
resistance to purine analogues, such as, for example, 6-
dimethylaminopurine, a need for L-methionine, optionally a
30 partial and compensable need for L-isoleucine, a need for
meso-diaminopimelic acid, auxotrophy in respect of
threonine-containing dipeptides, resistance to L-threonine,
resistance to L-homoserine, resistance to L-lysine,
resistance to L-methionine, resistance to L-glutamic acid,

resistance to L-aspartate, resistance to L-leucine, resistance to L-phenylalanine, resistance to L-serine, resistance to L-cysteine, resistance to L-valine, sensitivity to fluoropyruvate, defective threonine

5 dehydrogenase, optionally an ability for sucrose utilization, enhancement of the threonine operon, enhancement of homoserine dehydrogenase I-aspartate kinase I, preferably of the feed back resistant form, enhancement of homoserine kinase, enhancement of threonine synthase,

10 enhancement of aspartate kinase, optionally of the feed back resistant form, enhancement of aspartate semialdehyde dehydrogenase, enhancement of phosphoenol pyruvate carboxylase, optionally of the feed back resistant form, enhancement of phosphoenol pyruvate synthase, enhancement

15 of transhydrogenase, enhancement of the RhtB gene product, enhancement of the RhtC gene product, enhancement of the YfiK gene product, enhancement of a pyruvate carboxylase, and attenuation of acetic acid formation.

It has been found that microorganisms of the

20 Enterobacteriaceae family produce L-amino acids, in particular L-threonine, in an improved manner after enhancement, in particular over-expression, of the male gene.

The nucleotide sequences of the genes of *Escherichia coli*

25 belong to the prior art and can also be found in the genome sequence of *Escherichia coli* published by Blattner et al. (Science 277: 1453-1462 (1997)).

The following information, inter alia, on the male gene is known from the prior art:

30 Description: Periplasmic binding protein for maltose transport

Reference: Duplay et al.; Journal of Biological Chemistry 259(16): 10606-10613 (1984);

Dassa and Lambert; Research in Microbiology
148(5): 389-395 (1997); Quiocho et al.;
Structure 5(8): 997-1015 (1997)

Accession No.: AE000476

5 Alternative gene name: malB

The nucleic acid sequences can be found in the databanks of the National Center for Biotechnology Information (NCBI) of the National Library of Medicine (Bethesda, MD, USA), the nucleotide sequence databank of the European Molecular 10 Biologies Laboratories (EMBL, Heidelberg, Germany or Cambridge, UK) or the DNA databank of Japan (DDBJ, Mishima, Japan).

The genes described in the text references mentioned can be used according to the invention. Alleles of the genes which 15 result from the degeneracy of the genetic code or due to "sense mutations" of neutral function can furthermore be used.

To achieve an enhancement, for example, expression of the genes or the catalytic properties of the proteins can be 20 increased. The two measures can optionally be combined.

To achieve an over-expression, the number of copies of the corresponding genes can be increased, or the promoter and regulation region or the ribosome binding site upstream of the structural gene can be mutated. Expression cassettes 25 which are incorporated upstream of the structural gene act in the same way. By inducible promoters, it is additionally possible to increase the expression in the course of fermentative L-threonine production. The expression is likewise improved by measures to prolong the 30 life of the m-RNA. Furthermore, the enzyme activity is also increased by preventing the degradation of the enzyme protein. The genes or gene constructs can either be present in plasmids with a varying number of copies, or can be integrated and amplified in the chromosome.

Alternatively, an over-expression of the genes in question can furthermore be achieved by changing the composition of the media and the culture procedure.

Instructions in this context can be found by the expert,

5 inter alia, in Chang and Cohen (Journal of Bacteriology 134: 1141-1156 (1978)), in Hartley and Gregori (Gene 13: 347-353 (1981)), in Amann and Brosius (Gene 40: 183-190 (1985)), in de Broer et al. (Proceedings of the National Academy of Sciences of the United States of America 80: 21-10 25 (1983)), in LaVallie et al. (BIO/TECHNOLOGY 11: 187-193 (1993)), in PCT/US97/13359, in Llosa et al. (Plasmid 26: 222-224 (1991)), in Quandt and Klipp (Gene 80: 161-169 (1989)), in Hamilton et al. (Journal of Bacteriology 171: 4617-4622 (1989)), in Jensen and Hammer (Biotechnology and 15 Bioengineering 58: 191-195 (1998)) and in known textbooks of genetics and molecular biology.

Plasmid vectors which are capable of replication in Enterobacteriaceae, such as e.g. cloning vectors derived from pACYC184 (Bartolomé et al.; Gene 102: 75-78 (1991)), 20 pTrc99A (Amann et al.; (Gene 69: 301-315 (1988)) or pSC101 derivatives (Vocke and Bastia; Proceedings of the National Academy of Sciences of the United States of America 80 (21): 6557-6561 (1983)) can be used. A strain transformed with a plasmid vector, where the plasmid vector carries at 25 least the malE gene, or the nucleotide sequence which codes for this, can be employed in a process according to the invention.

It is also possible to transfer mutations which affect the expression of the particular gene into various strains by 30 sequence exchange (Hamilton et al.; Journal of Bacteriology 171: 4617-4622 (1989)), conjugation or transduction.

It may furthermore be advantageous for the production of L-amino acids, in particular L-threonine, with strains of the Enterobacteriaceae family, in addition to enhancement of

the *malE* gene, for one or more enzymes of the known threonine biosynthesis pathway or enzymes of anaplerotic metabolism or enzymes for the production of reduced nicotinamide adenine dinucleotide phosphate or enzymes of 5 glycolysis or PTS enzymes or enzymes of sulfur metabolism to be enhanced.

Thus, for example, at the same time one or more of the genes chosen from the group consisting of

- the *thrABC* operon which codes for aspartate kinase, 10 homoserine dehydrogenase, homoserine kinase and threonine synthase (US-A-4,278,765),
- the *pyc* gene of *Corynebacterium glutamicum* which codes for pyruvate carboxylase (WO 99/18228),
- the *pps* gene which codes for phosphoenol pyruvate 15 synthase (Molecular and General Genetics 231(2): 332-336 (1992)),
- the *ppc* gene which codes for phosphoenol pyruvate carboxylase (Gene 31: 279-283 (1984)),
- the *pntA* and *pntB* genes which code for transhydrogenase 20 (European Journal of Biochemistry 158: 647-653 (1986)),
- the *rhtB* gene which imparts homoserine resistance (EP-A-0 994 190),
- the *mgo* gene which codes for malate:quinone 25 oxidoreductase (WO 02/06459),
- the *rhtC* gene which imparts threonine resistance (EP-A-1 013 765),
- the *thrE* gene of *Corynebacterium glutamicum* which codes for the threonine export protein (WO 01/92545),

- the *gdhA* gene which codes for glutamate dehydrogenase (Nucleic Acids Research 11: 5257-5266 (1983); Gene 23: 199-209 (1983)),
- the *hns* gene which codes for the DNA-binding protein 5 HLP-II (Molecular and General Genetics 212: 199-202 (1988)),
- the *pgm* gene which codes for phosphoglucomutase (Journal of Bacteriology 176: 5847-5851 (1994)),
- the *fba* gene which codes for fructose biphosphate 10 aldolase (Biochemical Journal 257: 529-534 (1989)),
- the *ptsH* gene of the *ptsHICrr* operon which codes for the phosphohistidine protein hexose phosphotransferase of the phosphotransferase system PTS (Journal of Biological Chemistry 262: 16241-16253 (1987)),
- 15 • the *ptsI* gene of the *ptsHICrr* operon which codes for enzyme I of the phosphotransferase system PTS (Journal of Biological Chemistry 262: 16241-16253 (1987)),
- the *crr* gene of the *ptsHICrr* operon which codes for the glucose-specific IIA component of the phosphotransferase 20 system PTS (Journal of Biological Chemistry 262: 16241-16253 (1987)),
- the *ptsG* gene which codes for the glucose-specific IIBC component (Journal of Biological Chemistry 261: 16398-16403 (1986)),
- 25 • the *lrp* gene which codes for the regulator of the leucine regulon (Journal of Biological Chemistry 266: 10768-10774 (1991)),
- the *mopB* gene which codes for 10 Kd chaperone (Journal of Biological Chemistry 261: 12414-12419 (1986)) and is 30 also known by the name *groES*,

- the ahpC gene of the ahpCF operon which codes for the small sub-unit of alkyl hydroperoxide reductase (Proceedings of the National Academy of Sciences of the United States of America 92: 7617-7621 (1995)),
- 5 • the ahpF gene of the ahpCF operon which codes for the large sub-unit of alkyl hydroperoxide reductase (Proceedings of the National Academy of Sciences of the United States of America 92: 7617-7621 (1995)),
- 10 • the cysK gene which codes for cysteine synthase A (Journal of Bacteriology 170: 3150-3157 (1988)),
- the cysB gene which codes for the regulator of the cys regulon (Journal of Biological Chemistry 262: 5999-6005 (1987)),
- 15 • the cysJ gene of the cysJIH operon which codes for the flavoprotein of NADPH sulfite reductase (Journal of Biological Chemistry 264: 15796-15808 (1989), Journal of Biological Chemistry 264: 15726-15737 (1989)),
- 20 • the cysI gene of the cysJIH operon which codes for the haemoprotein of NADPH sulfite reductase (Journal of Biological Chemistry 264: 15796-15808 (1989), Journal of Biological Chemistry 264: 15726-15737 (1989)),
- 25 • the cysH gene of the cysJIH operon which codes for adenylyl sulfate reductase (Journal of Biological Chemistry 264: 15796-15808 (1989), Journal of Biological Chemistry 264: 15726-15737 (1989)),
- the phoB gene of the phoBR operon which codes for the positive regulator PhoB of the pho regulon (Journal of Molecular Biology 190 (1): 37-44 (1986)),
- 30 • the phoR gene of the phoBR operon which codes for the sensor protein of the pho regulon (Journal of Molecular Biology 192 (3): 549-556 (1986)),

- the phoE gene which codes for protein E of the outer cell membrane (Journal of Molecular Biology 163 (4): 513-532 (1983)),
- the pykF gene which codes for fructose-stimulated 5 pyruvate kinase I (Journal of Bacteriology 177 (19): 5719-5722 (1995)),
- the pfkB gene which codes for 6-phosphofructokinase II (Gene 28 (3): 337-342 (1984)),
- the talB gene which codes for transaldolase B (Journal 10 of Bacteriology 177 (20): 5930-5936 (1995)),
- the rseA gene of the rseABC operon which codes for a membrane protein with anti-sigmaE activity (Molecular Microbiology 24 (2): 355-371 (1997)),
- the rseC gene of the rseABC operon which codes for a 15 global regulator of the sigmaE factor (Molecular Microbiology 24 (2): 355-371 (1997)),
- the sodA gene which codes for superoxide dismutase (Journal of Bacteriology 155 (3): 1078-1087 (1983)),
- the sucA gene of the sucABCD operon which codes for the 20 decarboxylase sub-unit of 2-ketoglutarate dehydrogenase (European Journal of Biochemistry 141 (2): 351-359 (1984)),
- the sucB gene of the sucABCD operon which codes for the 25 dihydrolipoyltranssuccinase E2 sub-unit of 2-ketoglutarate dehydrogenase (European Journal of Biochemistry 141 (2): 361-374 (1984)),
- the sucC gene of the sucABCD operon which codes for the β -sub-unit of succinyl-CoA synthetase (Biochemistry 24 (22): 6245-6252 (1985)) and

- the sucD gene of the sucABCD operon which codes for the α -sub-unit of succinyl-CoA synthetase (Biochemistry 24 (22): 6245-6252 (1985)),

can be enhanced, in particular over-expressed.

5 It may furthermore be advantageous for the production of L-amino acids, in particular L-threonine, in addition to enhancement of the malE gene, for one or more of the genes chosen from the group consisting of

- the tdh gene which codes for threonine dehydrogenase (Journal of Bacteriology 169: 4716-4721 (1987)),
- the mdh gene which codes for malate dehydrogenase (E.C. 1.1.1.37) (Archives in Microbiology 149: 36-42 (1987)),
- the gene product of the open reading frame (orf) yjfA (Accession Number AAC77180 of the National Center for Biotechnology Information (NCBI, Bethesda, MD, USA)),
- the gene product of the open reading frame (orf) ytfP (Accession Number AAC77179 of the National Center for Biotechnology Information (NCBI, Bethesda, MD, USA)),
- the pckA gene which codes for the enzyme phosphoenol pyruvate carboxykinase (Journal of Bacteriology 172: 7151-7156 (1990)),
- the poxB gene which codes for pyruvate oxidase (Nucleic Acids Research 14(13): 5449-5460 (1986)),
- the aceA gene which codes for the enzyme isocitrate lyase (Journal of Bacteriology 170: 4528-4536 (1988)),
- the dgsA gene which codes for the DgsA regulator of the phosphotransferase system (Bioscience, Biotechnology and Biochemistry 59: 256-251 (1995)) and is also known under the name of the mlc gene,

- the fruR gene which codes for the fructose repressor (Molecular and General Genetics 226: 332-336 (1991)) and is also known under the name of the cra gene and
- the rpoS gene which codes for the sigma³⁸ factor (WO 5 01/05939) and is also known under the name of the katF gene,

to be attenuated, in particular eliminated or for the expression thereof to be reduced.

The term "attenuation" in this connection describes the 10 reduction or elimination of the intracellular activity of one or more enzymes (proteins) in a microorganism which are coded by the corresponding DNA, for example by using a weak promoter or a gene or allele which codes for a corresponding enzyme with a low activity or inactivates the 15 corresponding enzyme (protein) or gene, and optionally combining these measures.

By attenuation measures, the activity or concentration of the corresponding protein is in general reduced to 0 to 75%, 0 to 50%, 0 to 25%, 0 to 10% or 0 to 5% of the 20 activity or concentration of the wild-type protein or of the activity or concentration of the protein in the starting microorganism.

It may furthermore be advantageous for the production of L-amino acids, in particular L-threonine, in addition to 25 enhancement of the malE gene, to eliminate undesirable side reactions (Nakayama: "Breeding of Amino Acid Producing Microorganisms", in: Overproduction of Microbial Products, Krumphanzl, Sikyta, Vanek (eds.), Academic Press, London, UK, 1982).

30 The microorganisms produced according to the invention can be cultured in the batch process (batch culture), the fed batch process (feed process) or the repeated fed batch process (repetitive feed process). A summary of known

culture methods is described in the textbook by Chmiel (Bioprozesstechnik 1. Einführung in die Bioverfahrenstechnik [Bioprocess Technology 1. Introduction to Bioprocess Technology (Gustav Fischer Verlag, Stuttgart, 5 1991)) or in the textbook by Storhas (Bioreaktoren und periphere Einrichtungen [Bioreactors and Peripheral Equipment] (Vieweg Verlag, Braunschweig/Wiesbaden, 1994)).

The culture medium to be used must meet the requirements of the particular strains in a suitable manner. Descriptions 10 of culture media for various microorganisms are contained in the handbook "Manual of Methods for General Bacteriology" of the American Society for Bacteriology (Washington D.C., USA, 1981).

Sugars and carbohydrates, such as e.g. glucose, sucrose, 15 lactose, fructose, maltose, molasses, starch and optionally cellulose, oils and fats, such as e.g. soya oil, sunflower oil, groundnut oil and coconut fat, fatty acids, such as e.g. palmitic acid, stearic acid and linoleic acid, alcohols, such as e.g. glycerol and ethanol, and organic 20 acids, such as e.g. acetic acid, can be used as the source of carbon. These substances can be used individually or as a mixture.

Organic nitrogen-containing compounds, such as peptones, yeast extract, meat extract, malt extract, corn steep 25 liquor, soya bean flour and urea, or inorganic compounds, such as ammonium sulfate, ammonium chloride, ammonium phosphate, ammonium carbonate and ammonium nitrate, can be used as the source of nitrogen. The sources of nitrogen can be used individually or as a mixture.

30 Phosphoric acid, potassium dihydrogen phosphate or dipotassium hydrogen phosphate or the corresponding sodium-containing salts can be used as the source of phosphorus. The culture medium must furthermore comprise salts of metals, such as e.g. magnesium sulfate or iron sulfate,

which are necessary for growth. Finally, essential growth substances, such as amino acids and vitamins, can be employed in addition to the abovementioned substances.

Suitable precursors can moreover be added to the culture

5 medium. The starting substances mentioned can be added to the culture in the form of a single batch, or can be fed in during the culture in a suitable manner.

Basic compounds, such as sodium hydroxide, potassium hydroxide, ammonia or aqueous ammonia, or acid compounds,

10 such as phosphoric acid or sulfuric acid, can be employed in a suitable manner to control the pH of the culture.

Antifoams, such as e.g. fatty acid polyglycol esters, can be employed to control the development of foam. Suitable substances having a selective action, e.g. antibiotics, can

15 be added to the medium to maintain the stability of plasmids. To maintain aerobic conditions, oxygen or oxygen-containing gas mixtures, such as e.g. air, are introduced into the culture. The temperature of the culture is usually 25°C to 45°C, and preferably 30°C to

20 40°C. Culturing is continued until a maximum of L-amino acids or L-threonine has formed. This target is usually reached within 10 hours to 160 hours.

The analysis of L-amino acids can be carried out by anion exchange chromatography with subsequent ninhydrin

25 derivation, as described by Spackman et al. (Analytical Chemistry 30: 1190-1206 (1958)), or it can take place by reversed phase HPLC as described by Lindroth et al. (Analytical Chemistry 51: 1167-1174 (1979)).

The process according to the invention is used for the 30 fermentative preparation of L-amino acids, such as, for example, L-threonine, L-isoleucine, L-valine, L-methionine, L-homoserine and L-lysine, in particular L-threonine.

The present invention is explained in more detail in the following with the aid of embodiment examples.

The minimal (M9) and complete media (LB) for Escherichia coli used are described by J.H. Miller (A Short Course in Bacterial Genetics (1992), Cold Spring Harbor Laboratory Press). The isolation of plasmid DNA from Escherichia coli 5 and all techniques of restriction, ligation, Klenow and alkaline phosphatase treatment are carried out by the method of Sambrook et al. (Molecular Cloning - A Laboratory Manual (1989) Cold Spring Harbor Laboratory Press). Unless described otherwise, the transformation of Escherichia coli 10 is carried out by the method of Chung et al. (Proceedings of the National Academy of Sciences of the United States of America 86: 2172-2175 (1989)).

The incubation temperature for the preparation of strains and transformants is 37°C.

15 Example 1

Construction of the expression plasmid pTrc99Amale

The male gene from E. coli K12 is amplified using the polymerase chain reaction (PCR) and synthetic oligonucleotides. Starting from the nucleotide sequence of 20 the male gene in E. coli K12 MG1655 (Accession Number AE000476, Blattner et al. (Science 277: 1453-1462 (1997))), PCR primers are synthesized (MWG Biotech, Ebersberg, Germany). The sequences of the primers are modified such that recognition sites for restriction enzymes are formed. 25 The recognition sequence for SacI is chosen for the male1 primer and the recognition sequence for StuI for the male2 primer, which are marked by underlining in the nucleotide sequence shown below:

male1: 5' - TCACGAGCTTCACCAACTAGGACCATAG - 3' (SEQ ID No. 30 1)

male2: 5' - CGTCTTATCAGGCTACATACG - 3' (SEQ ID No. 2)

The chromosomal *E. coli* K12 MG1655 DNA employed for the PCR is isolated according to the manufacturer's instructions with "Qiagen Genomic-tips 100/G" (QIAGEN, Hilden, Germany). A DNA fragment approx. 1300 bp in size can be amplified

5 with the specific primers under standard PCR conditions (Innis et al. (1990) PCR Protocols. A guide to methods and applications, Academic Press) with Pfu-DNA polymerase (Promega Corporation, Madison, USA). The PCR product is cleaved with the restriction enzymes SacI and StuI and

10 ligated with the vector pTrc99A (Pharmacia Biotech, Uppsala, Sweden), which has been digested with the enzymes SacI and SmaI. The *E. coli* strain XL1-Blue MRF' (Stratagene, La Jolla, USA) is transformed with the ligation batch and plasmid-carrying cells are selected on

15 LB agar, to which 50 µg/ml ampicillin are added. Successful cloning can be demonstrated after plasmid DNA isolation by control cleavage with the enzymes PauI, PvuI, SspI and StyI. The plasmid is called pTrc99Amale (Figure 1).

Example 2

20 Preparation of L-threonine with the strain
MG442/pTrc99Amale

The L-threonine-producing *E. coli* strain MG442 is described in the patent specification US-A- 4,278,765 and deposited as CMIM B-1628 at the Russian National Collection for
25 Industrial Microorganisms (VKPM, Moscow, Russia).

The strain MG442 is transformed with the expression plasmid pTrc99Amale described in example 1 and with the vector pTrc99A and plasmid-carrying cells are selected on LB agar with 50 µg/ml ampicillin. The strains MG442/pTrc99Amale and
30 MG442/pTrc99A are formed in this manner. Selected individual colonies are then multiplied further on minimal medium with the following composition: 3.5 g/l Na₂HPO₄·2H₂O, 1.5 g/l KH₂PO₄, 1 g/l NH₄Cl, 0.1 g/l MgSO₄·7H₂O, 2 g/l glucose, 20 g/l agar, 50 mg/l ampicillin. The formation of

L-threonine is checked in batch cultures of 10 ml contained in 100 ml conical flasks. For this, 10 ml of preculture medium of the following composition: 2 g/l yeast extract, 10 g/l $(\text{NH}_4)_2\text{SO}_4$, 1 g/l KH_2PO_4 , 0.5 g/l $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 15 g/l 5 CaCO_3 , 20 g/l glucose, 50 mg/l ampicillin are inoculated and the batch is incubated for 16 hours at 37°C and 180 rpm on an ESR incubator from Kühner AG (Birsfelden, Switzerland).

250 μl portions of this preculture are transinoculated into 10 10 ml of production medium (25 g/l $(\text{NH}_4)_2\text{SO}_4$, 2 g/l KH_2PO_4 , 1 g/l $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 0.03 g/l $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 0.018 g/l $\text{MnSO}_4 \cdot 1\text{H}_2\text{O}$, 30 g/l CaCO_3 , 20 g/l glucose, 50 mg/l ampicillin) and the batch is incubated for 48 hours at 37°C. The formation of L-threonine by the starting strain MG442 is investigated in 15 the same manner, but no addition of ampicillin to the medium takes place. After the incubation the optical density (OD) of the culture suspension is determined with an LP2W photometer from Dr. Lange (Düsseldorf, Germany) at a measurement wavelength of 660 nm.

20 The concentration of L-threonine formed is then determined in the sterile-filtered culture supernatant with an amino acid analyzer from Eppendorf-BioTronik (Hamburg, Germany) by ion exchange chromatography and post-column reaction with ninhydrin detection.

25 The result of the experiment is shown in Table 1.

Table 1

Strain	OD (660 nm)	L-Threonine g/l
MG442	5.6	1.4
MG442/pTrc99A	3.8	1.3
MG442/pTrc99AmaleE	5.0	2.4

Brief Description of the Figure:

Figure 1: Map of the plasmid pTrc99AmaleE containing the
5 maleE gene.

The length data are to be understood as approx. data. The abbreviations and designations used have the following meaning:

- Amp: Ampicillin resistance gene
- 10 • lacI: Gene for the repressor protein of the trc promoter
- P_{trc}: trc promoter region, IPTG-inducible
- maleE: Coding region of the maleE gene
- 5S: 5S rRNA region
- 15 • rrnBT: rRNA terminator region

The abbreviations for the restriction enzymes have the following meaning

- PauI: Restriction endonuclease from *Paracoccus alcaliphilus*

- *PvuI*: Restriction endonuclease from *Proteus vulgaris* (ATCC 13315)
- *SacI*: Restriction endonuclease from *Streptomyces achromogenes* (ATCC 12767)
- 5 • *SspI*: Restriction endonuclease from *Sphaerotilus* species ATCC 13925
- *StyI*: Restriction endonuclease from *Salmonella typhi*

What is claimed is:

1. A process for the preparation of L-amino acids, in particular L-threonine, which comprises carrying out the following steps:
 - 5 a) fermentation of microorganisms of the Enterobacteriaceae family which produce the desired L-amino acid and in which at least the malE gene, or the nucleotide sequence which codes for this, is enhanced, in particular over-expressed,
 - 10 b) concentration of the desired L-amino acid in the medium or in the cells of the microorganisms, and
 - 15 c) isolation of the desired L-amino acid, constituents of the fermentation broth and/or the biomass in its entirety or portions (> 0 to 100%) thereof optionally remaining in the product.
2. A process as claimed in claim 1, wherein microorganisms in which further genes of the biosynthesis pathway of the desired L-amino acid are additionally enhanced are employed.
- 20 3. A process as claimed in claim 1, wherein microorganisms in which the metabolic pathways which reduce the formation of the desired L-amino acid are at least partly eliminated are employed.
4. A process as claimed in claim 1, wherein the expression of the polynucleotide which codes for the malE gene is increased.
- 25 5. A process as claimed in claim 1, wherein the regulatory and/or catalytic properties of the polypeptide (protein) for which the polynucleotide malE codes are improved or increased.

6. A process as claimed in claim 1, wherein, for the preparation of L-amino acids, microorganisms of the Enterobacteriaceae family in which in addition at the same time one or more of the genes chosen from the group consisting of:

5 6.1 the *thrABC* operon which codes for aspartate kinase, homoserine dehydrogenase, homoserine kinase and threonine synthase,

10 6.2 the *pyc* gene which codes for pyruvate carboxylase,

15 6.3 the *pps* gene which codes for phosphoenol pyruvate synthase,

6.4 the *ppc* gene which codes for phosphoenol pyruvate carboxylase,

15 6.5 the *pntA* and *pntB* genes which code for transhydrogenase,

20 6.6 the *rhtB* gene which imparts homoserine resistance,

6.7 the *mgo* gene which codes for malate:quinone oxidoreductase,

20 6.8 the *rhtC* gene which imparts threonine resistance,

6.9 the *thrE* gene which codes for the threonine export protein,

25 6.10 the *gdhA* gene which codes for glutamate dehydrogenase,

6.11 the *hns* gene which codes for the DNA-binding protein HLP-II,

- 6.12 the *pgm* gene which codes for phosphoglucomutase,
- 6.13 the *fba* gene which codes for fructose biphosphate aldolase,
- 5 6.14 the *ptsH* gene which codes for the phosphohistidine protein hexose phosphotransferase,
- 6.15 the *ptsI* gene which codes for enzyme I of the phosphotransferase system,
- 10 6.16 the *crr* gene which codes for the glucose-specific IIA component,
- 6.17 the *ptsG* gene which codes for the glucose-specific IIBC component,
- 15 6.18 the *lrp* gene which codes for the regulator of the leucine regulon,
- 6.19 the *mopB* gene which codes for 10 Kd chaperone,
- 6.20 the *ahpC* gene which codes for the small sub-unit of alkyl hydroperoxide reductase,
- 20 6.21 the *ahpF* gene which codes for the large sub-unit of alkyl hydroperoxide reductase,
- 6.22 the *cysK* gene which codes for cysteine synthase A,
- 6.23 the *cysB* gene which codes for the regulator of the *cys* regulon,
- 25 6.24 the *cysJ* gene which codes for the flavoprotein of NADPH sulfite reductase,
- 6.25 the *cysI* gene which codes for the haemoprotein of NADPH sulfite reductase,

- 6.26 the cysH gene which codes for adenylyl sulfate reductase,
- 6.27 the phoB gene which codes for the positive regulator PhoB of the pho regulon,
- 5 6.28 the phoR gene which codes for the sensor protein of the pho regulon,
- 6.29 the phoE gene which codes for protein E of outer cell membrane,
- 10 6.30 the pykF gene which codes for fructose-stimulated pyruvate kinase I,
- 6.31 the pfkB gene which codes for 6-phosphofructokinase II,
- 6.32 the talB gene which codes for transaldolase B,
- 15 6.33 the rseA gene which codes for a membrane protein which acts as a negative regulator on sigmaE activity;
- 6.34 the rseC gene which codes for a global regulator of the sigmaE factor,
- 20 6.35 the sodA gene which codes for superoxide dismutase,
- 6.36 the sucA gene which codes for the decarboxylase sub-unit of 2-ketoglutarate dehydrogenase,
- 25 6.37 the sucB gene which codes for the dihydrolipoyltranssuccinase E2 sub-unit of 2-ketoglutarate dehydrogenase,
- 6.38 the sucC gene which codes for the β -sub-unit of succinyl-CoA synthetase,

6.39 the *sucD* gene which codes for the α -sub-unit of succinyl-CoA synthetase,

is or are enhanced, in particular over-expressed, are fermented.

5 7. A process as claimed in claim 1, wherein, for the preparation of L-amino acids, microorganisms of the Enterobacteriaceae family in which in addition at the same time one or more of the genes chosen from the group consisting of:

10 7.1 the *tdh* gene which codes for threonine dehydrogenase,

7.2 the *mdh* gene which codes for malate dehydrogenase,

15 7.3 the gene product of the open reading frame (orf) *yjfa*,

7.4 the gene product of the open reading frame (orf) *ytfP*,

7.5 the *pckA* gene which codes for phosphoenol pyruvate carboxykinase,

20 7.6 the *poxB* gene which codes for pyruvate oxidase,

7.7 the *aceA* gene which codes for isocitrate lyase,

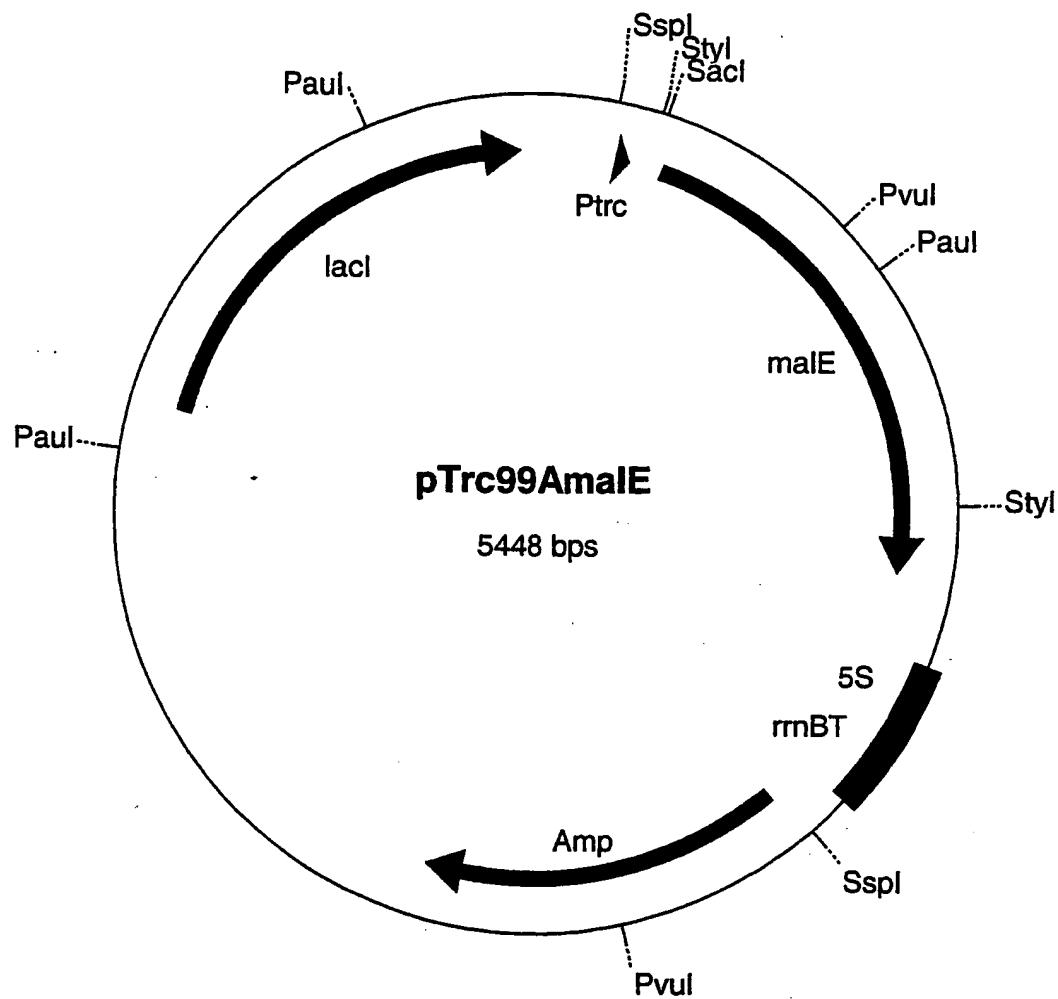
7.8 the *dgsA* gene which codes for the *DgsA* regulator of the phosphotransferase system,

25 7.9 the *fruR* gene which codes for the fructose repressor,

7.10 the *rpoS* gene which codes for the σ^{38} factor

is or are attenuated, in particular eliminated or reduced in expression, are fermented.

Figure 1:



SEQUENCE PROTOCOL

5 <110> Degussa AG

10 <120> Process for the preparation of L-amino acids using
 strains of the Enterobacteriaceae family which contain an
 enhanced maleE gene

15 <130> 020275BT

20 <160> 2

25 <170> PatentIn version 3.1

30 <210> 1

35 <211> 30

40 <212> DNA

45 <213> artificial sequence

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65 <223> maleE1

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80 30

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105 <220>

110 <221> Primer

115 <222> (1)..(22)

120 <223> maleE2

125 <400> 2

130 cgtcttatca ggcctacata cg

135 22

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LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,
MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG,
SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ,
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— of inventorship (Rule 4.17(iv)) for US only

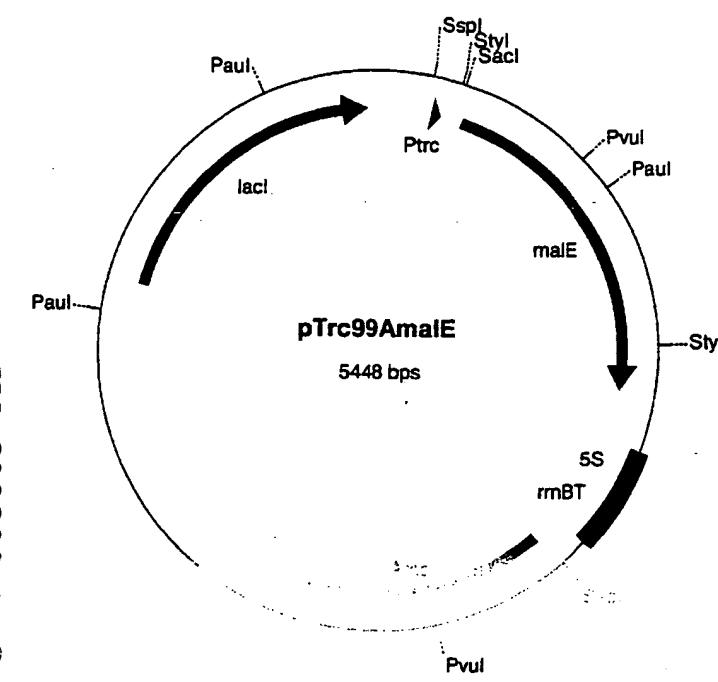
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(54) Title: PROCESS FOR THE PREPARATION OF L-AMINO ACIDS USING STRAINS OF THE ENTEROBACTERIACEAE FAMILY WHICH CONTAIN AN ENHANCED MALE GENE



(57) Abstract: The invention relates to a process for the preparation of L-amino acids, in particular L-threonine, in which the following steps are carried out: a) fermentation of microorganisms of the Enterobacteriaceae family which produce the desired L-amino acid and in which at least the malE gene, or the nucleotide sequence which codes for this, is or are enhanced, in particular over-expressed, b) concentration of the desired L-amino acid in the medium or in the cells of the bacteria, and c) isolation of the desired L-amino acid.

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B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
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Patent family members are listed in annex.

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van de Kamp, M

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E	WO 03 008607 A (RIEPING MECHTHILD ;DEGUSSA (DE)) 30 January 2003 (2003-01-30) the whole document claims 1,6 ---	1-7
E	WO 03 008608 A (RIEPING MECHTHILD ;DEGUSSA (DE)) 30 January 2003 (2003-01-30) the whole document claims 1,6 ---	1-7
E	WO 03 008609 A (RIEPING MECHTHILD ;DEGUSSA (DE)) 30 January 2003 (2003-01-30) the whole document claims 1,6 ---	1-7
E	WO 03 008610 A (RIEPING MECHTHILD ;DEGUSSA (DE)) 30 January 2003 (2003-01-30) the whole document claims 1,6 ---	1-7
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